Supplemental Table 1a: Predicted target genes of artificial microRNAs and expression changes in amiRNA overexpressers compared to wild-type controls by microarray analyses.

Identifier	Common name	Fold reduction (gcRMA analysis)		
amiR-mads-1				
At2g45660	MADS-box protein SOC1	2.3		
At2g13210	MADS-box protein ANR1	2.2 (A)		
At5g65050	MADS-box protein MAF2	2.1 *		
At1g77080	MADS-box protein MAF1	1.4		
At4g37940	MADS-box protein	A in wild type		
At2g22630	MADS-box protein AGL17	A in wild type		
At5g54060	MADS-box protein MAF3	not on ATH1 array		
At5g09680	cytochrome b5	not on ATH1 array		
amiR-mads-2 (weak lines)				
At1g24260	MADS-box protein AGL9	4.0†*		
At1g26310	MADS-box protein CAL	1.7*		
At1g48360	expressed protein	upregulated		
At1g51890	leucine-rich repeat protein kinase	absent in analyzed tissue		
At1g69120	MADS-box protein APETALA1 (AP1; AGL7)	6.3†*		
At2g03710	MADS-box protein AGL3	1.5		
At2g42830	MADS-box protein AGL5	1.3*		
At2g45650	MADS-box protein AGL6	3.8†* (A)		
At3g01990	ACT domain-containing protein (ACR6)	absent in analyzed tissue		
At3g02310	MADS-box protein SEPALLATA2 (AGL4; SEP2)	3.7†*		
At3g45360	hypothetical protein	absent in analyzed tissue		
	MADS-box protein SHATTERPROOF 1 (AGL1;			
At3g58780	SHP1)	1.2		
At4g11880	MADS-box protein AGL14	absent in analyzed tissue		
At4g22950	MADS-box protein AGL19	absent in analyzed tissue		
At5g03060	expressed protein	1.6		
At5g15800	MADS-box protein SEPALLATA1 (AGL2; SEP1)	2.5†*		
At5g20240	MADS-box protein PISTILLATA (PI)	1.2		
At5g60910	MADS-box protein FRUITFULL (FUL; AGL8)	1.5		
At4g04394	hypothetical protein	not on ATH1 array		

	amiR-mads-2 (strong lines)			
At1g24260	MADS-box protein AGL9	10.6†*		
At1g26310	MADS-box protein CAL	1.2		
At1g48360	expressed protein	upregulated		
At1g51890	leucine-rich repeat protein kinase	absent in analyzed tissue		
At1g69120	MADS-box protein APETALA1 (AP1; AGL7)	6.5†*		
At2g03710	MADS-box protein AGL3	1.8†		
At2g42830	MADS-box protein AGL5	3.9†*		
At2g45650	MADS-box protein AGL6	5.1†* (A)		
At3g01990	ACT domain-containing protein (ACR6)	absent in analyzed tissue		
At3g02310	MADS-box protein SEPALLATA2 (AGL4; SEP2)	7.3†*		
At3g45360	hypothetical protein	absent in analyzed tissue		
	MADS-box protein SHATTERPROOF 1 (AGL1;			
At3g58780	SHP1)	2.5†		
At4g11880	MADS-box protein AGL14	absent in analyzed tissue		
At4g22950	MADS-box protein AGL19	absent in analyzed tissue		
At5g03060	expressed protein	1.4		
At5g15800	MADS-box protein SEPALLATA1 (AGL2; SEP1)	2.9 *		
At5g20240	MADS-box protein PISTILLATA (PI)	2.0†*		
At5g60910	MADS-box protein FRUITFULL (FUL; AGL8)	1.3		
At4g04394	hypothetical protein	not on ATH1 array		
amiR-lfy-1				
At5g61850	LFY	4.6†*		
	amiR-white-1			
At3g59400	GENOMES UNCOUPLED 4 (GUN4)	5.7†		
	amiR-white-2			
At3g59400	GENOMES UNCOUPLED 4 (GUN4)	20.5† (A)		

A: absent according to Affymetrix GCOS algorithm

†: significantly changed (logit-T, p < 0.025)

\*significant expression change according to Bayes *B*-statistic with >98% probability (assuming 1% of differentially expressed genes) (Smyth, G.K., Michaud, J., and Scott, H.S. (2005). Use of within-array replicate spots for assessing differential expression in microarray experiments. Bioinformatics 21, 2067-2075.).

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Supplemental Table 1b: Predicted target genes of artificial microRNAs and expression changes in amiRNA overexpressers compared to wild-type controls by qualitative RT-PCR.

Identifier	Common name	Reduction
	amiR-lfy-2	
At5g61850	LFY	not analyzed
	amiR-ft-1	
At1g65480	FLOWERING LOCUS T (FT)	yes
-	amiR-ft-2	
At1g65480	FLOWERING LOCUS T (FT)	yes
	amiR-trichome	
At5g53200	TRIPTYCHON (TRY)	not analyzed
At2g46410	CAPRICE (CPC)	not analyzed
At2g30420	ENHANCER OF TRY AND CPC (ETC2)	not analyzed
	amiR-yabby-1	
At1g23420	INNER NO OUTER (INO)	yes
At4g00180	YABBY3 (YAB3)	yes
At3g07060	hypothetical protein	not analyzed
At5g11950	put. lysine decarboxylase	not analyzed
At5g02910	F-box protein	not analyzed
-	amiR-yabby-2	
At1g69180	CRABS CLAW (CRC)	no